



IFWO

RAW SEQUENCE LISTING

DATE: 09/01/2004

PATENT APPLICATION: US/10/799,782

TIME: 13:01:12

Input Set : N:\Crf3\RULE60\10799782.raw

Output Set: N:\CRF4\09012004\J799782.raw

SEQUENCE LISTING

1 (1) GENERAL INFORMATION:

2 (i) APPLICANT: Ullrich, Axel

3 Risau, Werner

4 Millauer, Birgit

5 Gazit, Aviv

6 Levitzki, Alex

7 (ii) TITLE OF INVENTION: Flk-1 Is A Receptor For Vascular
8 Endothelial Growth Factor

9 (iii) NUMBER OF SEQUENCES: 6

10 (iv) CORRESPONDENCE ADDRESS:

11 (A) ADDRESSEE: Pennie & Edmonds

12 (B) STREET: 1155 Avenue of the Americas

13 (C) CITY: New York

14 (D) STATE: New York

15 (E) COUNTRY: U.S.A.

16 (F) ZIP: 10036-2711

17 (v) COMPUTER READABLE FORM:

18 (A) MEDIUM TYPE: Floppy disk

19 (B) COMPUTER: IBM PC compatible

20 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

21 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

22 (vi) CURRENT APPLICATION DATA:

C--> 23 (A) APPLICATION NUMBER: US/10/799,782

C--> 24 (B) FILING DATE: 15-Mar-2004

25 (C) CLASSIFICATION:

29 (vii) PRIOR APPLICATION DATA:

27 (A) APPLICATION NUMBER: US/09/766,678

28 (B) FILING DATE: 25-Jan-2001

30 (A) APPLICATION NUMBER: 08/193,829

31 (B) FILING DATE: 09-FEB-1994

32 (viii) ATTORNEY/AGENT INFORMATION:

33 (A) NAME: Coruzzi, Laura A.

34 (B) REGISTRATION NUMBER: 30,742

35 (C) REFERENCE/DOCKET NUMBER: 7683-060

36 (ix) TELECOMMUNICATION INFORMATION:

37 (A) TELEPHONE: (212)790-9090

38 (B) TELEFAX: (212)869-9741

39 (C) TELEX: 66141 PENNIE

40 (2) INFORMATION FOR SEQ ID NO: 1:

41 (i) SEQUENCE CHARACTERISTICS:

42 (A) LENGTH: 5470 base pairs

43 (B) TYPE: nucleic acid

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44          (C) STRANDEDNESS: unknown
45          (D) TOPOLOGY: unknown
W--> 46      (ii) MOLECULE TYPE: DNA
47          (ix) FEATURE:
48              (A) NAME/KEY: CDS
49              (B) LOCATION: 286..4386
50          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
51 TATAGGGCGA ATTGGGTACG GGACCCCCCT CGAGGTCGAC GGTATCGATA AGCTTGATAT      60
52 CGAATTTCGGG CCCAGACTGT GTCCCGCAGC CGGGATAACC TGGCTGACCC GATTCCGCGG      120
53 ACACCGCTGA CAGCCGCGGC TGGAGCCAGG GCGCCGGTGC CCCGCGCTCT CCCCAGGTCTT      180
54 GCGCTGCGGG GGCCATACCG CCTCTGTGAC TTCTTTGCGG GCCAGGGACG GAGAAGGAGT      240
55 CTGTGCCTGA GAAACTGGGC TCTGTGCCCA GGCGCGAGGT GCAGG ATG GAG AGC      294
56                                     Met Glu Ser
57                                     1
58 AAG GCG CTG CTA GCT GTC GCT CTG TGG TTC TGC GTG GAG ACC CGA GCC      342
59 Lys Ala Leu Leu Ala Val Ala Leu Trp Phe Cys Val Glu Thr Arg Ala
60      5      10      15
61 GCC TCT GTG GGT TTG ACT GGC GAT TTT CTC CAT CCC CCC AAG CTC AGC      390
62 Ala Ser Val Gly Leu Thr Gly Asp Phe Leu His Pro Pro Lys Leu Ser
63 20      25      30      35
64 ACA CAG AAA GAC ATA CTG ACA ATT TTG GCA AAT ACA ACC CTT CAG ATT      438
65 Thr Gln Lys Asp Ile Leu Thr Ile Leu Ala Asn Thr Thr Leu Gln Ile
66      40      45      50
67 ACT TGC AGG GGA CAG CGG GAC CTG GAC TGG CTT TGG CCC AAT GCT CAG      486
68 Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro Asn Ala Gln
69      55      60      65
70 CGT GAT TCT GAG GAA AGG GTA TTG GTG ACT GAA TGC GGC GGT GGT GAC      534
71 Arg Asp Ser Glu Glu Arg Val Leu Val Thr Glu Cys Gly Gly Gly Asp
72      70      75      80
73 AGT ATC TTC TGC AAA ACA CTC ACC ATT CCC AGG GTG GTT GGA AAT GAT      582
74 Ser Ile Phe Cys Lys Thr Leu Thr Ile Pro Arg Val Val Gly Asn Asp
75      85      90      95
76 ACT GGA GCC TAC AAG TGC TCG TAC CGG GAC GTC GAC ATA GCC TCC ACT      630
77 Thr Gly Ala Tyr Lys Cys Ser Tyr Arg Asp Val Asp Ile Ala Ser Thr
78 100      105      110      115
79 GTT TAT GTC TAT GTT CGA GAT TAC AGA TCA CCA TTC ATC GCC TCT GTC      678
80 Val Tyr Val Tyr Val Arg Asp Tyr Arg Ser Pro Phe Ile Ala Ser Val
81      120      125      130
82 AGT GAC CAG CAT GGC ATC GTG TAC ATC ACC GAG AAC AAG AAC AAA ACT      726
83 Ser Asp Gln His Gly Ile Val Tyr Ile Thr Glu Asn Lys Asn Lys Thr
84      135      140      145
85 GTG GTG ATC CCC TGC CGA GGG TCG ATT TCA AAC CTC AAT GTG TCT CTT      774
86 Val Val Ile Pro Cys Arg Gly Ser Ile Ser Asn Leu Asn Val Ser Leu
87      150      155      160
88 TGC GCT AGG TAT CCA GAA AAG AGA TTT GTT CCG GAT GGA AAC AGA ATT      822
89 Cys Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly Asn Arg Ile
90      165      170      175
91 TCC TGG GAC AGC GAG ATA GGC TTT ACT CTC CCC AGT TAC ATG ATC AGC      870
92 Ser Trp Asp Ser Glu Ile Gly Phe Thr Leu Pro Ser Tyr Met Ile Ser

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93	180	185	190	195	
94	TAT GCC GGC ATG GTC TTC TGT GAG GCA AAG ATC AAT GAT GAA ACC TAT				918
95	Tyr Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp Glu Thr Tyr				
96		200	205	210	
97	CAG TCT ATC ATG TAC ATA GTT GTG GTT GTA GGA TAT AGG ATT TAT GAT				966
98	Gln Ser Ile Met Tyr Ile Val Val Val Val Gly Tyr Arg Ile Tyr Asp				
99		215	220	225	
100	GTG ATT CTG AGC CCC CCG CAT GAA ATT GAG CTA TCT GCC GGA GAA AAA				1014
101	Val Ile Leu Ser Pro Pro His Glu Ile Glu Leu Ser Ala Gly Glu Lys				
102		230	235	240	
103	CTT GTC TTA AAT TGT ACA GCG AGA ACA GAG CTC AAT GTG GGG CTT GAT				1062
104	Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Leu Asp				
105		245	250	255	
106	TTC ACC TGG CAC TCT CCA CCT TCA AAG TCT CAT AAG AAG ATT GTA				1110
107	Phe Thr Trp His Ser Pro Ser Lys Ser His His Lys Lys Ile Val				
108	260	265	270	275	
109	AAC CGG GAT GTG AAA CCC TTT CCT GGG ACT GTG GCG AAG ATG TTT TTG				1158
110	Asn Arg Asp Val Lys Pro Phe Pro Gly Thr Val Ala Lys Met Phe Leu				
111		280	285	290	
112	AGC ACC TTG ACA ATA GAA AGT GTG ACC AAG AGT GAC CAA GGG GAA TAC				1206
113	Ser Thr Leu Thr Ile Glu Ser Val Thr Lys Ser Asp Gln Gly Glu Tyr				
114		295	300	305	
115	ACC TGT GTA GCG TCC AGT GGA CGG ATG ATC AAG AGA AAT AGA ACA TTT				1254
116	Thr Cys Val Ala Ser Ser Gly Arg Met Ile Lys Arg Asn Arg Thr Phe				
117		310	315	320	
118	GTC CGA GTT CAC ACA AAG CCT TTT ATT GCT TTC GGT AGT GGG ATG AAA				1302
119	Val Arg Val His Thr Lys Pro Phe Ile Ala Phe Gly Ser Gly Met Lys				
120		325	330	335	
121	TCT TTG GTG GAA GCC ACA GTG GGC AGT CAA GTC CGA ATC CCT GTG AAG				1350
122	Ser Leu Val Glu Ala Thr Val Gly Ser Gln Val Arg Ile Pro Val Lys				
123	340	345	350	355	
124	TAT CTC AGT TAC CCA GCT CCT GAT ATC AAA TGG TAC AGA AAT GGA AGG				1398
125	Tyr Leu Ser Tyr Pro Ala Pro Asp Ile Lys Trp Tyr Arg Asn Gly Arg				
126		360	365	370	
127	CCC ATT GAG TCC AAC TAC ACA ATG ATT GTT GGC GAT GAA CTC ACC ATC				1446
128	Pro Ile Glu Ser Asn Tyr Thr Met Ile Val Gly Asp Glu Leu Thr Ile				
129		375	380	385	
130	ATG GAA GTG ACT GAA AGA GAT GCA GGA AAC TAC ACG GTC ATC CTC ACC				1494
131	Met Glu Val Thr Glu Arg Asp Ala Gly Asn Tyr Thr Val Ile Leu Thr				
132		390	395	400	
133	AAC CCC ATT TCA ATG GAG AAA CAG AGC CAC ATG GTC TCT CTG GTT GTG				1542
134	Asn Pro Ile Ser Met Glu Lys Gln Ser His Met Val Ser Leu Val Val				
135		405	410	415	
136	AAT GTC CCA CCC CAG ATC GGT GAG AAA GCC TTG ATC TCG CCT ATG GAT				1590
137	Asn Val Pro Pro Gln Ile Gly Glu Lys Ala Leu Ile Ser Pro Met Asp				
138	420	425	430	435	
139	TCC TAC CAG TAT GGG ACC ATG CAG ACA TTG ACA TGC ACA GTC TAC GCC				1638
140	Ser Tyr Gln Tyr Gly Thr Met Gln Thr Leu Thr Cys Thr Val Tyr Ala				
141		440	445	450	

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142	AAC	CCT	CCC	CTG	CAC	CAC	ATC	CAG	TGG	TAC	TGG	CAG	CTA	GAA	GAA	GCC	1686
143	Asn	Pro	Pro	Leu	His	His	Ile	Gln	Trp	Tyr	Trp	Gln	Leu	Glu	Glu	Ala	
144				455					460					465			
145	TGC	TCC	TAC	AGA	CCC	GGC	CAA	ACA	AGC	CCG	TAT	GCT	TGT	AAA	GAA	TGG	1734
146	Cys	Ser	Tyr	Arg	Pro	Gly	Gln	Thr	Ser	Pro	Tyr	Ala	Cys	Lys	Glu	Trp	
147				470					475					480			
148	AGA	CAC	GTG	GAG	GAT	TTC	CAG	GGG	GGA	AAC	AAG	ATC	GAA	GTC	ACC	AAA	1782
149	Arg	His	Val	Glu	Asp	Phe	Gln	Gly	Gly	Asn	Lys	Ile	Glu	Val	Thr	Lys	
150				485					490					495			
151	AAC	CAA	TAT	GCC	CTG	ATT	GAA	GGA	AAA	AAC	AAA	ACT	GTA	AGT	ACG	CTG	1830
152	Asn	Gln	Tyr	Ala	Leu	Ile	Glu	Gly	Lys	Asn	Lys	Thr	Val	Ser	Thr	Leu	
153	500					505						510				515	
154	GTC	ATC	CAA	GCT	GCC	AAC	GTG	TCA	GCG	TTG	TAC	AAA	TGT	GAA	GCC	ATC	1878
155	Val	Ile	Gln	Ala	Ala	Asn	Val	Ser	Ala	Leu	Tyr	Lys	Cys	Glu	Ala	Ile	
156						520						525				530	
157	AAC	AAA	GCG	GGA	CGA	GGA	GAG	AGG	GTC	ATC	TCC	TTC	CAT	GTG	ATC	AGG	1926
158	Asn	Lys	Ala	Gly	Arg	Gly	Glu	Arg	Val	Ile	Ser	Phe	His	Val	Ile	Arg	
159						535						540				545	
160	GGT	CCT	GAA	ATT	ACT	GTG	CAA	CCT	GCT	GCC	CAG	CCA	ACT	GAG	CAG	GAG	1974
161	Gly	Pro	Glu	Ile	Thr	Val	Gln	Pro	Ala	Ala	Gln	Pro	Thr	Glu	Gln	Glu	
162						550						555				560	
163	AGT	GTG	TCC	CTG	TTG	TGC	ACT	GCA	GAC	AGA	AAT	ACG	TTT	GAG	AAC	CTC	2022
164	Ser	Val	Ser	Leu	Leu	Cys	Thr	Ala	Asp	Arg	Asn	Thr	Phe	Glu	Asn	Leu	
165						565						570				575	
166	ACG	TGG	TAC	AAG	CTT	GGC	TCA	CAG	GCA	ACA	TCG	GTC	CAC	ATG	GGC	GAA	2070
167	Thr	Trp	Tyr	Lys	Leu	Gly	Ser	Gln	Ala	Thr	Ser	Val	His	Met	Gly	Glu	
168	580					585						590				595	
169	TCA	CTC	ACA	CCA	GTT	TGC	AAG	AAC	TTG	GAT	GCT	CTT	TGG	AAA	CTG	AAT	2118
170	Ser	Leu	Thr	Pro	Val	Cys	Lys	Asn	Leu	Asp	Ala	Leu	Trp	Lys	Leu	Asn	
171						600						605				610	
172	GGC	ACC	ATG	TTT	TCT	AAC	AGC	ACA	AAT	GAC	ATC	TTG	ATT	GTG	GCA	TTT	2166
173	Gly	Thr	Met	Phe	Ser	Asn	Ser	Thr	Asn	Asp	Ile	Leu	Ile	Val	Ala	Phe	
174						615						620				625	
175	CAG	AAT	GCC	TCT	CTG	CAG	GAC	CAA	GGC	GAC	TAT	GTT	TGC	TCT	GCT	CAA	2214
176	Gln	Asn	Ala	Ser	Leu	Gln	Asp	Gln	Gly	Asp	Tyr	Val	Cys	Ser	Ala	Gln	
177						630						635				640	
178	GAT	AAG	AAG	ACC	AAG	AAA	AGA	CAT	TGC	CTG	GTC	AAA	CAG	CTC	ATC	ATC	2262
179	Asp	Lys	Lys	Thr	Lys	Lys	Arg	His	Cys	Leu	Val	Lys	Gln	Leu	Ile	Ile	
180						645						650				655	
181	CTA	GAG	CGC	ATG	GCA	CCC	ATG	ATC	ACC	GGA	AAT	CTG	GAG	AAT	CAG	ACA	2310
182	Leu	Glu	Arg	Met	Ala	Pro	Met	Ile	Thr	Gly	Asn	Leu	Glu	Asn	Gln	Thr	
183	660					665						670				675	
184	ACA	ACC	ATT	GGC	GAG	ACC	ATT	GAA	GTG	ACT	TGC	CCA	GCA	TCT	GGA	AAT	2358
185	Thr	Thr	Ile	Gly	Glu	Thr	Ile	Glu	Val	Thr	Cys	Pro	Ala	Ser	Gly	Asn	
186						680						685				690	
187	CCT	ACC	CCA	CAC	ATT	ACA	TGG	TTC	AAA	GAC	AAC	GAG	ACC	CTG	GTA	GAA	2406
188	Pro	Thr	Pro	His	Ile	Thr	Trp	Phe	Lys	Asp	Asn	Glu	Thr	Leu	Val	Glu	
189						695						700				705	
190	GAT	TCA	GGC	ATT	GTA	CTG	AGA	GAT	GGG	AAC	CGG	AAC	CTG	ACT	ATC	CGC	2454

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191	Asp	Ser	Gly	Ile	Val	Leu	Arg	Asp	Gly	Asn	Arg	Asn	Leu	Thr	Ile	Arg	
192			710					715					720				
193	AGG	GTG	AGG	AAG	GAG	GAT	GGA	GGC	CTC	TAC	ACC	TGC	CAG	GCC	TGC	AAT	2502
194	Arg	Val	Arg	Lys	Glu	Asp	Gly	Gly	Leu	Tyr	Thr	Cys	Gln	Ala	Cys	Asn	
195		725					730					735					
196	GTC	CTT	GGC	TGT	GCA	AGA	GCG	GAG	ACG	CTC	TTC	ATA	ATA	GAA	GGT	GCC	2550
197	Val	Leu	Gly	Cys	Ala	Arg	Ala	Glu	Thr	Leu	Phe	Ile	Ile	Glu	Gly	Ala	
198	740					745					750					755	
199	CAG	GAA	AAG	ACC	AAC	TTG	GAA	GTC	ATT	ATC	CTC	GTC	GGC	ACT	GCA	GTG	2598
200	Gln	Glu	Lys	Thr	Asn	Leu	Glu	Val	Ile	Ile	Leu	Val	Gly	Thr	Ala	Val	
201				760						765					770		
202	ATT	GCC	ATG	TTC	TTC	TGG	CTC	CTT	CTT	GTC	ATT	GTC	CTA	CGG	ACC	GTT	2646
203	Ile	Ala	Met	Phe	Phe	Trp	Leu	Leu	Leu	Val	Ile	Val	Leu	Arg	Thr	Val	
204				775						780					785		
205	AAG	CGG	GCC	AAT	GAA	GGG	GAA	CTG	AAG	ACA	GGC	TAC	TTG	TCT	ATT	GTC	2694
206	Lys	Arg	Ala	Asn	Glu	Gly	Glu	Lys	Thr	Gly	Tyr	Leu	Ser	Ile	Val		
207			790					795				800					
208	ATG	GAT	CCA	GAT	GAA	TTG	CCC	TTG	GAT	GAG	CGC	TGT	GAA	CGC	TTG	CCT	2742
209	Met	Asp	Pro	Asp	Glu	Leu	Pro	Leu	Asp	Glu	Arg	Cys	Glu	Arg	Leu	Pro	
210		805					810					815					
211	TAT	GAT	GCC	AGC	AAG	TGG	GAA	TTC	CCC	AGG	GAC	CGG	CTG	AAA	CTA	GGA	2790
212	Tyr	Asp	Ala	Ser	Lys	Trp	Glu	Phe	Pro	Arg	Asp	Arg	Leu	Lys	Leu	Gly	
213	820					825					830					835	
214	AAA	CCT	CTT	GGC	CGC	GGT	GCC	TTC	GGC	CAA	GTG	ATT	GAG	GCA	GAC	GCT	2838
215	Lys	Pro	Leu	Gly	Arg	Gly	Ala	Phe	Gly	Gln	Val	Ile	Glu	Ala	Asp	Ala	
216				840						845					850		
217	TTT	GGA	ATT	GAC	AAG	ACA	GCG	ACT	TGC	AAA	ACA	GTA	GCC	GTC	AAG	ATG	2886
218	Phe	Gly	Ile	Asp	Lys	Thr	Ala	Thr	Cys	Lys	Thr	Val	Ala	Val	Lys	Met	
219				855					860						865		
220	TTG	AAA	GAA	GGA	GCA	ACA	CAC	AGC	GAG	CAT	CGA	GCC	CTC	ATG	TCT	GAA	2934
221	Leu	Lys	Glu	Gly	Ala	Thr	His	Ser	Glu	His	Arg	Ala	Leu	Met	Ser	Glu	
222			870					875					880				
223	CTC	AAG	ATC	CTC	ATC	CAC	ATT	GGT	CAC	CAT	CTC	AAT	GTG	GTG	AAC	CTC	2982
224	Leu	Lys	Ile	Leu	Ile	His	Ile	Gly	His	His	Leu	Asn	Val	Val	Asn	Leu	
225		885					890					895					
226	CTA	GGC	GCC	TGC	ACC	AAG	CCG	GGA	GGG	CCT	CTC	ATG	GTG	ATT	GTG	GAA	3030
227	Leu	Gly	Ala	Cys	Thr	Lys	Pro	Gly	Gly	Pro	Leu	Met	Val	Ile	Val	Glu	
228	900					905					910					915	
229	TTC	TGC	AAG	TTT	GGA	AAC	CTA	TCA	ACT	TAC	TTA	CGG	GGC	AAG	AGA	AAT	3078
230	Phe	Cys	Lys	Phe	Gly	Asn	Leu	Ser	Thr	Tyr	Leu	Arg	Gly	Lys	Arg	Asn	
231				920						925					930		
232	GAA	TTT	GTT	CCC	TAT	AAG	AGC	AAA	GGG	GCA	CGC	TTC	CGC	CAG	GGC	AAG	3126
233	Glu	Phe	Val	Pro	Tyr	Lys	Ser	Lys	Gly	Ala	Arg	Phe	Arg	Gln	Gly	Lys	
234				935					940						945		
235	GAC	TAC	GTT	GGG	GAG	CTC	TCC	GTG	GAT	CTG	AAA	AGA	CGC	TTG	GAC	AGC	3174
236	Asp	Tyr	Val	Gly	Glu	Leu	Ser	Val	Asp	Leu	Lys	Arg	Arg	Leu	Asp	Ser	
237			950					955					960				
238	ATC	ACC	AGC	AGC	CAG	AGC	TCT	GCC	AGC	TCA	GGC	TTT	GTT	GAG	GAG	AAA	3222
239	Ile	Thr	Ser	Ser	Gln	Ser	Ser	Ala	Ser	Ser	Gly	Phe	Val	Glu	Glu	Lys	

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L:23 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:24 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:46 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1
L:521 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3
L:531 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=4